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August 9, 2003, 16:23:48; Search time 48.0429 Seconds (without alignments) 102.055 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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sp_rvirus:*
sp_bacteriap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Ogited major raced	O80161 terrabacter	09vd73 aeropyrum p	Ogh4f3 orvza sativ	Ognd94 homo sapten	O69835 streptomyce	P72542 streptomyce	030370 pseudomonas	091115 pseudomonas		091211 streptomyce	~1	09zc02 streptomyce	08ft37 corvnebacte	c	
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Length DB	2027	127	144	187	238	284	292	327	328	334	485	493	501	507	514	524
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1716 1716 1717 1718 1718 1719 1719 1719 1719 1719	ALIGNMENTS RT; 2027 ated) t sequence t annotati	ruses:	ant N GenBa GenBa Soll. r. sel. 77B46
094243 094273 08W6U8 08U802 08V4A8 08U802 08V4A8 08FUN2 095384 081685 091685 091685 091814 089328 095289 092354 089359 094798 094798 069389 069389 069389	ALIGN PRT; Created) Last seq	-strand viruses, d-11289816; tion of the geno genus Maraflviru 01).	usigna EMBL/G EMBL/G LNAPO DS-PSO LDS-PSO Elicas elicas elicas elicas elicas elicas (el; 1.
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 100.
Matches 8; Conservative
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                  12 AARRAARA 19
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TISSUE-Uterus;
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Q8H4F3;
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"Phthalate catabolic gene cluster is linked to the angular dioxygenase gene in Terrabacter sp. strain DBF63.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB084235; BAC54158.1; -.
Hypothetical protein.
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Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijian K., Nakazawa H.,
Takaniya M., Mauda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
prenarchaeon, Aeropyrum pernix KI.";
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Intrasporangiaceae; Terrabacter.
NCBI_TaxID=150395;
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                Indels
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SEQUENCE 127 AA; 13364 MW; 32979994948814EB CRC64;
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Hypothetical protein; Complete proteome.
SEQUENCE 144 AA; 14937 MW; 973D6C61A0449375 CRC64;
                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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 Pred. No. 34;
Mismatches
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100.0%; Pred. No. 21;
ative 0; Mismatches
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NCBI_TaxID=56636;
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
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hes 8; Conser
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Q8G161;
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Sasaki I., Matsumoto I., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.1%; Score 8; DB 10; Length 187;
100.0%; Pred. No. 28;
ive 0; Mismatches 0; Indels
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Submitted (OCT-2002)
Submitted (OCT-2002)
EMBL, APO04230; BAC20029.1;
SEQUENCE 187 AA; 20294 MW; 39B908C139E3A993 CRC64;
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ALB34319; CAD38988 1.; -
InterPro; IPR003961; FW_III.
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SMART; SM0060; FN3; 1.
Hypothetical protein.
SEQUENCE 238 AA; 25262 MW; C7300A7D5A9E3095 CRC64;
ol-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
072013_G04.13 protein.
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"Identification and analysis of genes from Streptomyces pristinaespiralis encoding enzymes involved in the biosynthesis of the 4-dimethylamino-L-phenylalanine precursor of pristinamycin I."; Mol. Microbiol. 23:191-202(1997).

EMBL; U60417; AAC44869.1; ...

EMBL; U60417; AAC44869.1; ...

INCEPTO: IPR00255; HemK.

InterPro: IPR00255; HemK.

InterPro: IPR00051; SAW bind.

TIGRRAMS: TIGR0051; SAW bind.

TIGRRAMS: TIGR00521; NG MTASE.

SEQUENCE 292 AA; 30850 MW; 7B55A8B8E19F29FC CRC64;
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J. Bacteriol. 181:4118-4124(1999).
EMBL: AF0022222: AAC21671.1;
SEQUENCE 327 AA; 37019 MW; 08286F3B127C9B8B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBL_TaxID=287;
                                                                                                                                                              MEDLINE-97197164, PubMed-9044253,
Blanc V., Gil P., Bamas-Jacques N., Lorenzon S., Zagorec M.,
Schleuniger J., Bisch D., Blanche F., Debussche L., Crouzet J.,
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MEDLINE-99315810; PubMed-10383985;
Stintzi A., Johnson Z., Stonehouse M., Ochsner U., Meyer J.M.,
Vasil M.L., Poole K.;
                                             Streptomyces pristinaespiralis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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01-AuG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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100.0%; Pred. No. 41;
tive 0; Mismatches
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Matches 8; Conservative
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                                                                                                    NCBI_TaxID=38300;
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030370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Bopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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STRAIN-A3(2) / M145;
MEDLINE-21996410; PubMed-12000953;
MEDLINE-21996410; PubMed-12000953;
Bentley S.D., Chater K.E., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Hopwood D.A.;
Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete genome sequence of the model actinomycete Streptomyces
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6
                                                                          01-AUG-1998 (TEXBLrel. 07, Created)
01-AUG-1998 (TEXBLrel. 07, Last sequence update)
01-AMR-2003 (TEXBLrel. 23, Last annotation update)
ABC-transporter ATP-binding protein.
SCOG647 OR SCIBS. 07.
Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.1%; Score 8; DB 16; Length 284;
100.0%; Pred. No. 40;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                STRAIN-A3(2);
Harris D., Taylor K.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases;
                                                                                                                                                                                                                                                                                                                                                                                                                     Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding; Complete proteome.
SEQUENCE 284 AA; 30082 MW; BFBDC99EC634EA94 CRC64;
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Last annotation update)
                                                                                                                                                                                                              Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coelicolor A3(2).";
Mature 471:141-147(2002).
EMBL, AL939126; CAA18881.1;
InterPro; IPR003593; AAA.ATPase.
InterPro; IPR003593; AAA.ATPase.
Fam; PF00005; ABC_tran; I.
ProDom; PD000006; ABC_tran; I.
SMART; SM00382; AAA; I.
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                                         PRT;
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MEDLINE-97000351; PubMed-8843436;
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(TrEMBLrel. 02, I
(TrEMBLrel. 23, I
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Best Local Similarity 100.0
Matches 8; Conservative
                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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01-MAR-2003
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P72542;
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RESULT 6
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MEDLINE-21996410; Pubhed-12000953; MEDLINE-21996410; Pubhed-12000953; MEDLINE-21996410; Pubhed-12000953; Bentley S.D., Chater R.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James A. Brown S., Chandra G., Chen C.W., Collins M., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Croin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kleser T., Larke L., Murthy L., Ollver K., O'Neil S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Watter T., Wletzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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Caenorhabditis elegans.
Eukaryota; hetazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2),";
Nature 417:141-147(2002).
EMBL: AL939106; CAB69664.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.

NCBI_TaxID=1902;
                                                                           42.1%; Score 8; DB 16; Length 334; ilarity 100.0%; Pred. No. 45; Conservative 0; Mismatches 0; Indels
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SEQUENCE 485 AA; 50944 MW; 63053A5803396D10 CRC64;
334 AA; 34769 MW; 16E60916304D2F85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-0NAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative membrane protein.
SC00692 OR SCF42.02C OR SCF42.02C...
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein Y110A2AM.1.
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ilarity 100.0%; Pred. No. 61;
Conservative 0; Mismatches
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MEDLINE-99069613; PubMed-9851916;
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306 ARARRAAA 313
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Best Local Similarity
Matches 8; Conservi
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    SEQUENCE
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UN MEDLINE-21395509; PubMed=11481432;

UN MEDLINE-21395509; PubMed=11481432;

A Barloy-Hubler F., Bower L., Capela D., Galibert F., Gouzy J.,

Barloy-Hubler F., Bower L., Capela D., Galibert F., Gouzy J.,

A Gurjal M., Bong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,

A Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

A Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;

A Nucleotide sequence and predicted functions of the entire

Sinorhizobium mellioti pSymA megaplasmid ";

RT Sinorhizobium mellioti pSymA megaplasmid ";

Exemp. As007208; Aak64799.1; -

DR EMBL; As007208; Aak64799.1; -

DR FEMBL; PRO03767; Idh.2.

DR Pfam; PP02615; Idh.2.

DR Pfam; PP02615; Idh.2.

DR Pfamid; Hypothetical protein; Complete proteome.
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STRAIN-ATCC 15692, PRO1;
MEDLINE-20437337, PubMed-10984043;
MEDLINE-20437337, PubMed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Raizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PRO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium.
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Rhizobium meliloti (Sinorhizobium meliloti).
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0; Mismatches
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last anno
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EMBL; AE004651; AAG05642.1; -.
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319 ARAARRAA 326
                             318 ARAARRAA 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVCA OR PA2254
                                                                                                                                                                                                                                                                                                        01-MAR-2001
01-MAR-2001
01-MAR-2002
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                                                                                                                                                                                                                             0911L5
0911L5;
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Q930Q4
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à g THE REAL PROPERTY OF THE PROPE

Gaps

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Indels

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Gaps

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507 AA.

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STRAIN-YS-314 / Jan 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
IKOO K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
Usuda Y., Sugimoto S.;
The entire genomic sequence of Corynebacterium efficiens YS-314.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AP00519; BAC18544.1;
EMBL, AP00519; BAC18544.1;
SEQUENCE 507 AA; 55464 MW; 5CB3F673AFC7C33A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
                                                                                                                                                        42.1%; Score 8; DB 16; Length 501; 100.0%; Pred. No. 63; 1.1ve 0; Mismatches 0; Indels
                     EMBL; M. 1939148; CARLELONGE, I. INTERPRO! LONGE.
INTERPRO; IPR001206; PA_PPBase.
Pfam; PF00781; DAGKC, I.
SMART; SM00014; acidPPc; I.
SWART; SM00046; DAGKC, I.
HYDOCHALICAL PROTAIN; COMPLETE PROTAECOME.
SEART; SM00086; DAGKC, I.
SPOOTENCE SOI AA; 52342 MW; F124CB7FD5302365 CRC64;
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Best Local Similarity 100.0
                                                                                                                                          Query Match
Best Local Similarity Luc.
8, Conservative
 Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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469 ARAARRAA 476
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Q8FT37
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicalor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=A3(2) / M145,
MEDLINE=2396410; PubMed=12000953;
MEDLINE=2396410; PubMed=12000953;
MEDLINE=2396410; PubMed=12000953;
MEDLINE=2396410; PubMed=12000953;
MEDLINE=2396410; PubMed=12000953;
MEDRIA S.D., Chater R.F., Cerdeno-Tarraga A.-M., Kleser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidadyo J., Hornsby T., Bowarth S.,
Huang C.-H., Kleser T., Larke L., Murphy L., Ollver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomyclaeae; Streptomyces. NCBL_raxID-1902;
                                                                                                                                                                                                                                             42.1%; Score 8; DB 5; Length 493;
100.0%; Pred. No. 62;
tive 0; Mismatches 0; Indels
                                                                     "The sequence of C. elegans cosmid Y110A2AM.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-A3(2);
Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                            Seeger K.J., Harris D.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                         092C02;
01-MAY-1999 (TIEMBLrel. 10, Created)
01-MAY-1999 (TIEMBLrel. 10, Last sequence update)
01-WAR-2003 (TIEMBLrel. 23, Last annotation update)
Hypothetical protein SC06511.
                                                                                                                                                                                                                                                                                                                                                                                                           501 AA.
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MEDLINE-97000351; PubMed-8843436;
Science 282:2012-2018(1998).
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Best Local Similarity 100.8
Matches 8; Conservative
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178 AARRAARA 185
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                            SEQUENCE FROM N.A. STRAIN-Bristol N2;
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Bopwood D.A.;
                                                          Smith A.;
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Q92C02
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SEQUENCE FROM N.A. Schulsel J., Brandt P., Fartmann B., Holland R., Schultte U., Adyn V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                  Gaps
                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungl; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
42.1%; Score 8; DB 16; Length 507; 100.0%; Pred. No. 63; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                     Q8XQQ3 PRELIMINARY; PRT;
Q8XQQ3;
01-MAR-2002 (TrEMBLrel. 20, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conserved hypothetical protein.
5E6.140.
Neurospora crassa.
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RP SEQUENCE FROM N.A.

RA German Neurospora genome project;

RL Submitted (JAN-2002) Cabe EMBL/GenBank/DDBJ databases.

RRBL; AL670004; CAD21255.1; ---

DR EMBL; AL670004; Zaf_C242.

DR SHART; SM000358; Zaf_C242.

DR PROSITE; PS000038; ZINC_FINGER_C242_1; 1.

KW Hypothetical protein.

SQ SEQUENCE 514 AA; 57259 WW; F03E63327C2407F3 CRC64;
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 Query Match
 42.1%;
 Score 8;
 DB 3;
 Length 514;

 Best Local Similarity 100.0%;
 Pred. No. 64;

 Matches 8;
 Conservative 0;
 Mismatches 0;
 Indels

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Db 232 RAARRAR 239
Search completed: August 9, 2003, 16:32:57
Job time : 50.0429 secs